

# SEQUENCE LISTING

<110> JAKOBSEN, Bent Karsten  
BOULTER, Jonathan Michael

<120> Multivalent T Cell Receptor Complexes

<130> 102286.410

<140> US 09/334,969

<141> 1999-06-17

<150> PCT/GB99 01583

<151> 1999-05-19

<150> GB 9810759.2

<151> 1998-05-19

<150> GB 9821129.5

<151> 1998-09-29

<160> 85

<170> PatentIn Ver. 2.1

<210> 1

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gene coding  
for human HLA-A2/flu matrix peptide restricted  
JM22 TCR alpha chain fused to c-jun leucine zipper  
domain.

<400> 1

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atgcaactac tagaacaag tcttcagttt ctaagcatcc aagagggaga aaatctcact 60
gtgtactgca actcctcaag tgttttttcc agcttacaat ggtacagaca ggagcctggg 120
gaaggtcctg tcttcctggt gacagtagtt acgggtggag aagtgaagaa gctgaagaga 180
ctaacttttc agtttggtga tgcaagaaag gacagttctc tccacatcac tgcggcccag 240
cctggtgata caggcctcta cctctgtgca ggagcgggaa gccaaggaaa tctcatcttt 300
ggaaaaggca ctaaactctc tggttaaacca aatatccaga accctgaccc tgccgtgtac 360
cagctgagag actctaaatc cagtgacaag tctgtctgcc tattcacga ttttgattct 420
caaacaaatg tgtcacaaag taaggattct gatgtgtata tcacagacaa aactgtgcta 480
gacatgaggt ctatggactt caagagcaac agtgctgtgg cctggagcaa caaatctgac 540
tttgcatgtg caaacgcctt caacaacagc attattccag aagacacctt cttccccagc 600
ccagaaagtt cccccggggg tagaatcgcc cggctggagg aaaaagtgaa aaccttgaaa 660
gctcagaact cggagctggc gtccacggcc aacatgctca gggaacaggt ggcacagctt 720
aaacagaaag tcatgaacta ctag                                     744

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210> 2

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid sequence of human HLA-A2/flu matrix peptide restricted JM22 TCR alpha chain fused to c-jun leucine zipper domain.

<400> 2

Met Gln Leu Leu Glu Gln Ser Pro Gln Phe Leu Ser Ile Gln Glu Gly  
1 5 10 15

Glu Asn Leu Thr Val Tyr Cys Asn Ser Ser Ser Val Phe Ser Ser Leu  
20 25 30

Gln Trp Tyr Arg Gln Glu Pro Gly Glu Gly Pro Val Leu Leu Val Thr  
35 40 45

Val Val Thr Gly Gly Glu Val Lys Lys Leu Lys Arg Leu Thr Phe Gln  
50 55 60

Phe Gly Asp Ala Arg Lys Asp Ser Ser Leu His Ile Thr Ala Ala Gln  
65 70 75 80

Pro Gly Asp Thr Gly Leu Tyr Leu Cys Ala Gly Ala Gly Ser Gln Gly  
85 90 95

Asn Leu Ile Phe Gly Lys Gly Thr Lys Leu Ser Val Lys Pro Asn Ile  
100 105 110

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser  
115 120 125

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val  
130 135 140

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu  
145 150 155 160

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser  
165 170 175

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile  
180 185 190

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Pro Gly Gly Arg  
195 200 205

Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser  
210 215 220

Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu  
225 230 235 240

Lys Gln Lys Val Met Asn Tyr

<210> 3  
 <211> 864  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gene coding  
 for human HLA-A2/flu matrix peptide restricted  
 JM22 TCR beta chain fused to c-fos leucine zipper  
 domain.

<400> 3

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atggtggatg gtggaatcac tcagtcccca aagtacctgt tcagaaagga aggacagaat 60
gtgaccctga gttgtgaaca gaatttgaac cacgatgcca tgtactggta ccgacaggac 120
ccagggaag ggctgagatt gatctactac tcacagatag taaatgactt tcagaaagga 180
gatatagctg aagggtacag cgtctctcgg gagaagaagg aatcctttcc tctcactgtg 240
acatcgcccc aaaagaaccc gacagctttc tatctctgtg ccagtagttc gaggagctcc 300
tacgagcagt acttcggggc gggcaccagg ctcacggtea cagaggacct gaaaaacgtt 360
tccccacccg aggtcgctgt gtttgaacca tcagaagcag agatctccca caccacaaag 420
gccacactgg tgtgcctggc cacaggcttc taccocgacc acgtggagct gagctggtgg 480
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagccctt caaggagcag 540
ccgcctctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 600
tggcagaacc cccgcaacca ctcccgctgt caagtccagt tctacgggct ctcggagaat 660
gacgagtggg cccaggatag ggccaaacct gtcaccaga tcgtcagcgc cgaggcctgg 720
ggtagagcag accccggggg tctgactgat acactccaag cggagacaga tcaacttgaa 780
gacaagaagt ctgcgttgca gaccgagatt gccaatctac tgaaagagaa ggaaaaacta 840
gagttcatcc tggcagctta ctac                                     864

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<210> 4  
 <211> 287  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
 sequence of human HLA-A2/flu matrix peptide  
 restricted JM22 TCR beta chain fused to c-fos  
 leucine zipper domain.

<400> 4

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Met Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg Lys
  1              5              10              15

Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His Asp
      20              25              30

Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu Ile
      35              40              45

Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala Glu

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|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |
| Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr Val |     |     |     |     |
| 65  |     | 70  |     | 80  |
| Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser Ser |     |     |     |     |
|   | 85  |     | 90  | 95  |
| Ser Arg Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr |     |     |     |     |
|   | 100 |     | 105 | 110 |
| Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe |     |     |     |     |
|   | 115 |     | 120 | 125 |
| Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val |     |     |     |     |
|   | 130 |     | 135 | 140 |
| Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp |     |     |     |     |
| 145   |     | 150 |     | 155 |
| Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro |     |     |     |     |
|   | 165 |     | 170 | 175 |
| Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser |     |     |     |     |
|   | 180 |     | 185 | 190 |
| Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe |     |     |     |     |
|   | 195 |     | 200 | 205 |
| Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr |     |     |     |     |
|   | 210 |     | 215 | 220 |
| Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp |     |     |     |     |
| 225   |     | 230 |     | 235 |
| Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr |     |     |     |     |
|   | 245 |     | 250 | 255 |
| Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn |     |     |     |     |
|   | 260 |     | 265 | 270 |
| Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr     |     |     |     |     |
|   | 275 |     | 280 | 285 |

<210> 5  
 <211> 918  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gene coding  
 for human HLA-A2/flu matrix peptide restricted  
 JM22 TCR beta chain fused to c-fos leucine zipper

domain and BirA biotinylation tag.

<400> 5

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atggtggatg gtggaatcac tcagtcccca aagtacctgt tcagaaagga aggacagaat 60
gtgacctga gttgtgaaca gaatttgaac cacgatgcc a tgtactggta ccgacaggac 120
ccagggcaag ggctgagatt gatctactac tcacagatag taaatgactt tcagaaagga 180
gatatagctg aaggggtacag cgtctctcgg gagaagaagg aatcctttcc tctcactgtg 240
acatcggccc aaaagaaccc gacagctttc tatctctgtg ccagtagttc gaggagctcc 300
tacgagcagt acttcggggc gggcaccagg ctcacgggtc a cagaggacct gaaaaacgtt 360
tccccacccg aggtcgctgt gtttgaacca tcagaagcag agatctccca caccctaaag 420
gccacactgg tgtgcctggc cacaggcttc taccctgacc acgtggagct gagctggtgg 480
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagccct caaggagcag 540
cccgcctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 600
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcgagaaat 660
gacgagtgga cccaggatag ggccaaacct gtcaccacga tcgtcagcgc cgaggcctgg 720
ggtagagcag accccggggg tctgactgat aactccaag cggagacaga tcaacttgaa 780
gacaagaagt ctgcgttgca gaccgagatt gccaatctac tgaaagagaa ggaaaaacta 840
gagttcatcc tggcagctta cggatccggt ggtggtctga acgatatttt tgaagctcag 900
aaaatcgaat ggcattaa                                     918

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<210> 6

<211> 305

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of human HLA-A2/flu matrix peptide  
restricted JM22 TCR beta chain fused to c-fos  
leucine zipper domain and BirA biotinylation tag.

<400> 6

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Met Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg Lys
  1              5              10              15

Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His Asp
      20              25              30

Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu Ile
      35              40              45

Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala Glu
      50              55              60

Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr Val
      65              70              75              80

Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser Ser
      85              90              95

Ser Arg Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
      100             105             110

Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe

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|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 115   |     | 120 |     | 125 |
| Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val |     |     |     |     |
| 130   |     | 135 |     | 140 |
| Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp |     |     |     |     |
| 145   |     | 150 |     | 155 |
| Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro |     |     |     |     |
|   | 165 |     | 170 | 175 |
| Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser |     |     |     |     |
|   | 180 |     | 185 | 190 |
| Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe |     |     |     |     |
|   | 195 |     | 200 | 205 |
| Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr |     |     |     |     |
|   | 210 |     | 215 | 220 |
| Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp |     |     |     |     |
|   | 225 |     | 230 | 235 |
| Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr |     |     |     |     |
|   | 245 |     | 250 | 255 |
| Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn |     |     |     |     |
|   | 260 |     | 265 | 270 |
| Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr Gly |     |     |     |     |
|   | 275 |     | 280 | 285 |
| Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp |     |     |     |     |
|   | 290 |     | 295 | 300 |
| His   |     |     |     |     |
| 305   |     |     |     |     |

<210> 7  
 <211> 750  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gene coding  
 for human HLA-A2/HTLV-1 Tax peptide restricted TCR  
 alpha chain from clone A6 fused to c-jun leucine  
 zipper domain.

<400> 7  
 atgcagaagg aagtggagca gaactctgga cccctcagtg ttccagaggg agccattgcc 60  
 tctctcaact gcacttacag tgaccgaggt tcccagtcct tcttctggta cagacaatat 120  
 tctgggaaaa gccctgagtt gataatgtcc atatactcca atgggtgacaa agaagatgga 180

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aggtttacag cacagctcaa taaagccagc cagtatgttt ctctgctcat cagagactcc 240
cagcccagtg attcagccac ctacctctgt gccgttacaa ctgacagctg ggggaaattg 300
cagtttgag cagggacca ggttggtgac accccagata tccagaaccc tgaccctgcc 360
gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt 420
gattctcaaa caaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact 480
gtgctagaca tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa 540
tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc 600
cccagcccag aaagttcccc cgggggtaga atcgcccggc tggaggaaaa agtgaaaacc 660
ttgaaagctc agaactcgga gctggcgtcc acggccaaca tgctcaggga acaggtggca 720
cagcttaaac agaaagtcac gaactactag 750

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<210> 8  
 <211> 249  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Amino acid  
 sequence of human HLA-A2/HTLV-1 Tax peptide  
 restricted TCR alpha chain from clone A6 fused to  
 c-jun leucine zipper domain.

<400> 8  
 Met Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu  
 1 5 10 15  
 Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln  
 20 25 30  
 Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile  
 35 40 45  
 Met Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala  
 50 55 60  
 Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser  
 65 70 75 80  
 Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Thr Thr Asp Ser  
 85 90 95  
 Trp Gly Lys Leu Gln Phe Gly Ala Gly Thr Gln Val Val Val Thr Pro  
 100 105 110  
 Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys  
 115 120 125  
 Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr  
 130 135 140  
 Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr  
 145 150 155 160  
 Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala

|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 165 |  | 170 |  | 175 |
| Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser |     |  |     |  |     |
|   | 180 |  | 185 |  | 190 |
| Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Pro Gly |     |  |     |  |     |
|   | 195 |  | 200 |  | 205 |
| Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln |     |  |     |  |     |
|   | 210 |  | 215 |  | 220 |
| Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala |     |  |     |  |     |
|   | 225 |  | 230 |  | 235 |
|   |     |  |     |  | 240 |
| Gln Leu Lys Gln Lys Val Met Asn Tyr                             |     |  |     |  |     |
|   | 245 |  |     |  |     |

<210> 9  
 <211> 928  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Gene coding  
 for human HLA-A2/HTLV-1 Tax peptide restricted TCR  
 beta chain from clone A6 fused to c-fos leucine  
 zipper domain and BirA biotinylation tag.

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 aactgcagtg gtgcccagga tatgaaccat gaatacatgt cctgggtatcg acaagaccca 120  
 ggcattggggc tgaggctgat tcattactca gttgggtgctg gtatcactga ccaaggagaa 180  
 gtccccaatg gctacaatgt ctccagatca accacagagg atttcccgtc caggctgctg 240  
 tcggctgctc cctcccagac atctgtgtac ttctgtgcca gcaggccggg actagcggga 300  
 gggcgaccag agcagtactt cgggcccgggc accagggtca cggtcacaga ggacctgaaa 360  
 aacgtgttcc caccgaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc 420  
 caaaaggcca cactggtgtg cctggccaca ggcttctacc ccgaccacgt ggagctgagc 480  
 tgggtgggtga atgggaagga ggtgcacagt ggggtcagca cagaccgcga gcccctcaag 540  
 gagcagcccg cctcaatga ctccagatac gctctgagca gccgcctgag ggtctcggcc 600  
 accttctggc agaacccccg caaccacttc cgctgtcaag tccagttcta cgggctctcg 660  
 gagaatgacg agtggaccca ggatagggcc aaacctgtca cccagatcgt cagcgccgag 720  
 gcctggggta gagcagaccc cgggggtctg actgatacac tccaagcgga gacagatcaa 780  
 cttgaagaca agaagtctgc gttgcagacc gagattgcca atctactgaa agagaaggaa 840  
 aaactagagt tcattcctggc agcttacgga tccgggtggtg gtctgaacga tatttttgaa 900  
 gctcagaaaa tcgaatggca ttaagctt 928

<210> 10  
 <211> 307  
 <212> PRT  
 <213> Artificial Sequence

<220>



<223> Description of Artificial Sequence:Amino acid  
sequence of human HLA-A2/HTLV-1 Tax peptide  
restricted TCR beta chain from clone A6 fused to  
c-fos leucine zipper domain and BirA biotinylation  
tag.

<400> 10

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ala | Gly | Val | Thr | Gln | Thr | Pro | Lys | Phe | Gln | Val | Leu | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gln | Ser | Met | Thr | Leu | Gln | Cys | Ala | Gln | Asp | Met | Asn | His | Glu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ser | Trp | Tyr | Arg | Gln | Asp | Pro | Gly | Met | Gly | Leu | Arg | Leu | Ile | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ser | Val | Gly | Ala | Gly | Ile | Thr | Asp | Gln | Gly | Glu | Val | Pro | Asn | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Asn | Val | Ser | Arg | Ser | Thr | Thr | Glu | Asp | Phe | Pro | Leu | Arg | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ala | Ala | Pro | Ser | Gln | Thr | Ser | Val | Tyr | Phe | Cys | Ala | Ser | Arg | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Ala | Gly | Gly | Arg | Pro | Glu | Gln | Tyr | Phe | Gly | Pro | Gly | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Val | Thr | Glu | Asp | Leu | Lys | Asn | Val | Phe | Pro | Pro | Glu | Val | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Phe | Glu | Pro | Ser | Glu | Ala | Glu | Ile | Ser | His | Thr | Gln | Lys | Ala | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Cys | Leu | Ala | Thr | Gly | Phe | Tyr | Pro | Asp | His | Val | Glu | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Trp | Val | Asn | Gly | Lys | Glu | Val | His | Ser | Gly | Val | Ser | Thr | Asp | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Pro | Leu | Lys | Glu | Gln | Pro | Ala | Leu | Asn | Asp | Ser | Arg | Tyr | Ala | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Arg | Leu | Arg | Val | Ser | Ala | Thr | Phe | Trp | Gln | Asn | Pro | Arg | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Phe | Arg | Cys | Gln | Val | Gln | Phe | Tyr | Gly | Leu | Ser | Glu | Asn | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Trp | Thr | Gln | Asp | Arg | Ala | Lys | Pro | Val | Thr | Gln | Ile | Val | Ser | Ala | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ala | Trp | Gly | Arg | Ala | Asp | Pro | Gly | Gly | Leu | Thr | Asp | Thr | Leu | Gln | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |

Glu Thr Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile  
260 265 270

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
275 280 285

Tyr Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile  
290 295 300

Glu Trp His  
305

<210> 11  
<211> 765  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Gene coding  
for human HLA-A2/HTLV-1 Tax peptide restricted TCR  
alpha chain from clone M10B7/D3 fused to c-jun  
leucine zipper domain.

<400> 11  
atgcaacaga agaattgatga ccagcaagtt aagcaaaaatt caccatccct gagcgtccag 60  
gaaggaagaa tttctattct gaactgtgac tatactaaca gcatgtttga ttatttccta 120  
tggtacaaaa aataccctgc tgaaggtcct acattcctga tatctataag ttccattaag 180  
gataaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct 240  
ctgcacattg tgccctccca gcctggagac tctgcagtgt acttctgtgc agcaatggag 300  
ggagcccaga agctggtatt tggccaagga accaggctga ctatcaaccc aaatatccag 360  
aaccctgacc ctgccgtgta ccagctgaga gactctaaat ccagtgcaca gtctgtctgc 420  
ctattcaccg attttgattc tcaaacaaat gtgtcacaaa gtaaggattc tgatgtgtat 480  
atcacagaca aaactgtgct agacatgagg tctatggact tcaagagcaa cagtgtctgtg 540  
gcctggagca acaaattctga ctttgcattg gcaaacgcct tcaacaacag cattattcca 600  
gaagacacct tcttccccag cccagaaaagt tcccccgagg gtagaatcgc ccggtctggag 660  
gaaaaagtga aaaccttgaa agctcagaac tccggagctgg cgtccacggc caacatgctc 720  
agggaaacagg tggcacagct taaacagaaa gtcattgaact actag 765

<210> 12  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Amino acid  
sequence of human HLA-A2/HTLV-1 Tax peptide  
restricted TCR alpha chain from clone M10B7/D3  
fused to c-jun leucine zipper domain

<400> 12  
Met Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln Asn Ser Pro Ser  
1 5 10 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Val | Gln | Glu | Gly | Arg | Ile | Ser | Ile | Leu | Asn | Cys | Asp | Tyr | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     | 30  |     |     |     |     |     |
| Asn | Ser | Met | Phe | Asp | Tyr | Phe | Leu | Trp | Tyr | Lys | Lys | Tyr | Pro | Ala | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     | 45  |     |     |     |     |     |
| Gly | Pro | Thr | Phe | Leu | Ile | Ser | Ile | Ser | Ser | Ile | Lys | Asp | Lys | Asn | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |
| Asp | Gly | Arg | Phe | Thr | Val | Phe | Leu | Asn | Lys | Ser | Ala | Lys | His | Leu | Ser |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     |     |     |
| Leu | His | Ile | Val | Pro | Ser | Gln | Pro | Gly | Asp | Ser | Ala | Val | Tyr | Phe | Cys |
|     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |     |     |     |     |
| Ala | Ala | Met | Glu | Gly | Ala | Gln | Lys | Leu | Val | Phe | Gly | Gln | Gly | Thr | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     | 110 |     |     |     |     |     |
| Leu | Thr | Ile | Asn | Pro | Asn | Ile | Gln | Asn | Pro | Asp | Pro | Ala | Val | Tyr | Gln |
|     |     |     | 115 |     |     |     | 120 |     |     | 125 |     |     |     |     |     |
| Leu | Arg | Asp | Ser | Lys | Ser | Ser | Asp | Lys | Ser | Val | Cys | Leu | Phe | Thr | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     | 140 |     |     |     |     |     |
| Phe | Asp | Ser | Gln | Thr | Asn | Val | Ser | Gln | Ser | Lys | Asp | Ser | Asp | Val | Tyr |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     |     |     |
| Ile | Thr | Asp | Lys | Thr | Val | Leu | Asp | Met | Arg | Ser | Met | Asp | Phe | Lys | Ser |
|     |     |     | 165 |     |     |     | 170 |     |     | 175 |     |     |     |     |     |
| Asn | Ser | Ala | Val | Ala | Trp | Ser | Asn | Lys | Ser | Asp | Phe | Ala | Cys | Ala | Asn |
|     |     |     | 180 |     |     |     | 185 |     |     | 190 |     |     |     |     |     |
| Ala | Phe | Asn | Asn | Ser | Ile | Ile | Pro | Glu | Asp | Thr | Phe | Phe | Pro | Ser | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     | 205 |     |     |     |     |     |
| Glu | Ser | Ser | Pro | Gly | Gly | Arg | Ile | Ala | Arg | Leu | Glu | Glu | Lys | Val | Lys |
|     |     |     | 210 |     |     |     | 215 |     |     | 220 |     |     |     |     |     |
| Thr | Leu | Lys | Ala | Gln | Asn | Ser | Glu | Leu | Ala | Ser | Thr | Ala | Asn | Met | Leu |
|     |     |     | 225 |     |     |     | 230 |     |     | 235 |     |     |     |     |     |
| Arg | Glu | Gln | Val | Ala | Gln | Leu | Lys | Gln | Lys | Val | Met | Asn | Tyr |     |     |
|     |     |     | 245 |     |     |     | 250 |     |     |     |     |     |     |     |     |

<210> 13

<211> 925

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gene coding for human HLA-A2/HTLV-1 Tax peptide restricted TCR

beta chain from clone M10B7/D3 fused to c-fos  
leucine zipper domain and BirA biotinylation tag.

<400> 13

```

atgaacgctg gtgtcactca gacccccaaaa ttccaggtcc tgaagacagg acagagcatg 60
acactgcagt gtgcccagga tatgaaccat gaatacatgt cctggtatcg acaagaccca 120
ggcatggggc tgaggctgat tcattactca gttggtgctg gtatcactga ccaaggagaa 180
gtccccaatg gctacaatgt ctccagatca accacagagg atttcccgtc caggtctgctg 240
tcggctgctc cctcccagac atctgtgtac ttctgtgcca gcagttacca ggaggggggg 300
ttttacgagc agtacttcgg gccggggcacc aggtctacgg tcacagagga cctgaaaaac 360
gtgttcccac ccgaggtcgc tgtgtttgag ccatcagaag cagagatctc ccacacccaa 420
aaggccacac tgggtgtgcct ggccacaggc ttctaccccg accacgtgga gctgagctgg 480
tgggtgaatg ggaaggaggt gcacagtggg gtcagcacag acccgagcc cctcaaggag 540
cagcccgcgc tcaatgactc cagatacgtc ctgagcagcc gcctgagggt ctgggccacc 600
ttctggcagg acccccgcaa ccacttcgcg tgtcaagtcc agttctacgg gctctcggag 660
aatgacgagt ggacccagga tagggccaaa cccgtcaccc agatcgtcag cgccgaggcc 720
tggggtagag cagaccccgg ggggtctgact gatacactcc aagcggagac agatcaactt 780
gaagacaaga agtctgcgtt gcagaccgag attgccaatc tactgaaaga gaaggaaaaa 840
ctagagttca tcctggcagc ttacggatcc ggtggtggtc tgaacgatat ttttgaagct 900
cagaaaatcg aatggcatta agctt                                     925

```

<210> 14

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of human HLA-A2/HTLV-1 Tax peptide  
restricted TCR beta chain from cloneM10B7/D3 fused  
to c-fos leucine zipper domain and BirA  
biotinylation tag.

<400> 14

```

Met Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr
  1              5              10              15

Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr
          20              25              30

Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His
          35              40              45

Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn Gly
          50              55              60

Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu
          65              70              75              80

Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr
          85              90              95

Pro Gly Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu
          100              105              110

```

Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val  
 115 120 125  
 Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu  
 130 135 140  
 Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp  
 145 150 155 160  
 Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln  
 165 170 175  
 Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu Ser  
 180 185 190  
 Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn His  
 195 200 205  
 Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp  
 210 215 220  
 Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala  
 225 230 235 240  
 Trp Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu  
 245 250 255  
 Thr Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala  
 260 265 270  
 Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr  
 275 280 285  
 Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu  
 290 295 300  
 Trp His  
 305

<210> 15  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Forward poly-C  
 "anchor" primer for PCR amplification of cDNAs  
 extended at their 3'-terminal with a stretch of  
 G-residues using Terminal Transferase.

<400> 15  
 taaatactcg aggcgcgcc ccccccccc ccc

33

<210> 16  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Human TCR  
alpha chain constant region 3'-specific PCR  
primer.

<400> 16  
atataaccgc gggaaccaga tccccacagg aactttctgg gctgggga 48

<210> 17  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Human TCR beta  
chain constant region 3'-specific PCR primer.

<400> 17  
atataaccgc gggaaccaga tccccacagt ctgctctacc ccaggcc 47

<210> 18  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Human c-jun  
leucine zipper 5'-specific PCR primer.

<400> 18  
catcacccgc ggggtagaat cgcccggtg gag 33

<210> 19  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Human c-jun  
leucine zipper 3'-specific PCR primer.

<400> 19  
gtgtgtgtc gaggatccta gtagttcatg actttctgtt taagctgtgc 50

<210> 20  
<211> 39

<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human c-fos  
leucine zipper 5'-specific PCR primer.

<400> 20

catacacccg ggggtctgac tgatacactc caagcggag

39

<210> 21

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human c-fos  
leucine zipper 3'-specific PCR primer.

<400> 21

tgtgtgctcg aggatcctag taagctgcc a ggatgaactc tagtttttc

49

<210> 22

<211> 120

<212> DNA

<213> Homo sapiens

<220>

<223> Partial human c-jun sequence coding for the  
leucine zipper domain as fused to TCR alpha  
chains.

<400> 22

agaatcgccc ggctggagga aaaagtga aa accttgaaag ctcagaactc ggagctggcg 60  
tccacggcca acatgctcag ggaacaggtg gcacagctta aacagaaagt catgaactac 120

<210> 23

<211> 120

<212> DNA

<213> Homo sapiens

<220>

<223> Partial human c-fos sequence coding for the  
leucine zipper domain as fused to TCR beta chains.

<400> 23

ctgactgata cactccaagc ggagacagac caactagaag atgagaagtc tgctttgcag 60  
accgagattg ccaacctgct gaaggagaag gaaaaactag agttcatcct ggcagcttac 120

<210> 24

<211> 40

<212> PRT  
<213> Homo sapiens

<220>

<223> c-jun leucine zipperdomain amino acid sequence as  
fused to TCR alpha chains.

<400> 24

Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn  
1 5 10 15

Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln  
20 25 30

Leu Lys Gln Lys Val Met Asn Tyr  
35 40

<210> 25

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<223> c-fos leucine zipper domain amino acid sequence as  
fused to TCR beta chains.

<400> 25

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys  
1 5 10 15

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys  
20 25 30

Leu Glu Phe Ile Leu Ala Ala Tyr  
35 40

<210> 26

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward PCR  
primer for mutating the unpaired cysteine of human  
TCR beta chains to serine.

<400> 26

gactccagat acagcctgag cagccg

26

<210> 27



<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Partial amino acid sequence of the human TCR beta chain after mutating the unpaired cysteine to serine.

<400> 27  
Asp Ser Arg Tyr Ser Leu Ser Ser  
1 5

<210> 28  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Reverse PCR primer for mutating the unpaired cysteine of human TCR beta chains to serine.

<400> 28  
cggctgctca ggctgtatct ggagtc 26

<210> 29  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Forward PCR primer for mutating the unpaired cysteine of human TCR beta chains to alanine.

<400> 29  
gactccagat acgctctgag cagccg 26

<210> 30  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Partial amino acid sequence of the human TCR beta chain after mutating the unpaired cysteine to alanine.

<400> 30  
Asp Ser Arg Tyr Ala Leu Ser Ser

<210> 31  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Reverse PCR  
 primer for mutating the unpaired cysteine of human  
 TCR beta chains to alanine.

<400> 31  
 cggctgctca gagcgtatct ggagtc

26

<210> 32  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: 5' PCR primer  
 for the human v alpha10.2 chain of the JM22  
 Influenza matrix protein peptide/HLA-A0201  
 restricted TCR.

<400> 32  
 gctctagaca tatgcaacta ctagaacaaa gtcctcagtt tctaagcatc caagagg

57

<210> 33  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: New N-terminal  
 amino acid sequence of truncated Valpha10.2 chain  
 of the JM22 Influenza Matrix protein  
 peptide/HLA-A0201 restricted TCR.

<400> 33  
 Met Gln Leu Leu Glu Gln Ser Pro Gln Phe Leu Ser Ile Gln Glu  
 1 5 10 15

<210> 34  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' PCR primer  
for amplification of the human Vbeta17 chain of  
the JM22 Influenza matrix peptide/HLA-A0201  
restricted TCR.

<400> 34

gctctagaca tatggtggat ggtggaatca ctcaagtc

39

<210> 35

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: New  
N-terminal amino acid sequence of the truncated  
Vbeta17 chain of the human JM22 Influenza Matrix  
peptide/HLA-A0201 restricted TCR.

<400> 35

Met Val Asp Gly Gly Ile Thr Gln Ser

1

5

<210> 36

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' PCR primer  
for amplification of the mouse Valpha4 chain of  
the Influenza virus nucleoprotein peptide/H2-Db  
restricted TCR.

<400> 36

gctctagaca tatggattct gttactcaaa tgcaaggatca agtgaccctc tcatcag

57

<210> 37

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: New N-terminal  
amino acid sequence of truncated Valpha4 chain of  
the mouse Influenza virus nucleoprotein  
peptide/H2-Db restricted TCR.

<400> 37

Met Asp Ser Val Thr Gln Met Gln Gly Gln Val Thr Leu Ser Ser

1

5

10

15

&lt;210&gt; 38

&lt;211&gt; 53

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

<223> 5' PCR primer for amplification of the mouse  
Vbeta11 chain of the Influenza nucleoprotein  
peptide/H2-Db restricted TCR.

&lt;400&gt; 38

gctctagaca tatggaacca acaaatgctg gtgttatcca aacacctagg cac 53

&lt;210&gt; 39

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;220&gt;

<223> New N-terminal amino acid sequence of truncated  
Vbeta11 chain of the mouse Influenza virus  
nucleoprotein peptide/H2-Db restricted TCR.

&lt;400&gt; 39

Met Glu Pro Thr Asn Ala Gly Val Ile Gln Thr Pro Arg His

1

5

10

&lt;210&gt; 40

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> 5' PCR primer for amplification of the human  
Valpha23 chain of the HIV-1 Gag peptide/HLA-A0201  
restricted TCR.

&lt;400&gt; 40

ggaattccat atgaaacaag aggttacaca aattcc 36

&lt;210&gt; 41

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> New N-terminal amino acid sequence of truncated

human Valpha23 chain of the HIV-1 Gag  
peptide/HLA-A0201 restricted TCR.

<400> 41

Met Lys Gln Glu Val Thr Gln Ile

1

5

<210> 42

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> 5' PCR primer for amplification of the human  
Vbeta5.1 chain of the HIV-1 Gag peptide/HLA-A0201  
restricted TCR.

<400> 42

ggaattccat atgaaagctg gagttactca aactcc

36

<210> 43

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> New N-terminal amino acid sequence of truncated  
human Vbeta5.1 chain of the HIV-1 Gag  
peptide/HLA-A0201 restricted TCR.

<400> 43

Met Lys Ala Gly Val Thr Gln Thr

1

5

<210> 44

<211> 33

<212> DNA

<213> Homo sapiens

<220>

<223> 5' PCR primer for amplification of the human  
Valpha2.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted A6 TCR.

<400> 44

ccccccata tgcagaagga agtggagcag aac

33

<210> 45

<211> 8

<212> PRT  
<213> Homo sapiens

<220>

<223> New N-terminal amino acid sequence of truncated  
human Valpha2.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted A6 TCR.

<400> 45

Met Gln Lys Glu Val Glu Gln Lys  
1 5

<210> 46

<211> 33

<212> DNA

<213> Homo sapiens

<220>

<223> 5' PCR primer for amplification of the human  
Vbeta12.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted A6 TCR.

<400> 46

ccccccata tgaacgctgg tgtcactcag acc

33

<210> 47

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> New N-terminal amino acid sequence of truncated  
human Vbeta12.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted A6 TCR

<400> 47

Met Lys Ala Gly Val Thr Gln Thr  
1 5

<210> 48

<211> 48

<212> DNA

<213> Homo sapiens

<220>

<223> 5' PCR primer for amplification of the human  
Valpha17.2 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted B7 TCR.

<400> 48

ccccccata tgcaacaaaa aaatgatgac cagcaagtta agcaaaat

48

<210> 49

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> New N-terminal amino acid sequence of truncated  
human Valpha17.2 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted B7 TCR

<400> 49

Met Gln Gln Lys Asn Asp Asp Gln Gln Val Lys Gln Asn  
1 5 10

<210> 50

<211> 45

<212> DNA

<213> Homo sapiens

<220>

<223> 5' PCR primer for amplification of the human  
Vbeta12.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted B7 TCR.

<400> 50

ccccccata tgaacgctgg tgtcactcag accccaaaat tccag

45

<210> 51

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> New N-terminal amino acid sequence of truncated  
human Vbeta12.3 chain of the HTLV-1 Tax  
peptide/HLA-A0201 restricted B7 TCR

<400> 51

Met Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln  
1 5 10

<210> 52

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> 3' PCR primer for the human Calpha chains,  
generally applicable.

<400> 52

catacacccg ggggaacttt ctgggctggg gaagaagg

38

<210> 53

<211> 33

<212> DNA

<213> Homo sapiens

<220>

<223> 3' PCR primer for human Cbeta chains, generally  
applicable.

<400> 53

catacacccg ggggtctgctc taccacagggc etc

33

<210> 54

<211> 744

<212> DNA

<213> Homo sapiens

<220>

<223> Mutated DNA sequence of soluble HLA-A2/flu matrix  
restricted TCR alpha chain from JM22, as fused to  
the leucine zipper domain of human c-jun.

<400> 54

atgcaactac tagaacaag tcctcagttt ctaagcatcc aagagggaga aaatctcact 60  
gtgtactgca actcctcaag tgttttttcc agcttacaat ggtacagaca ggagcctggg 120  
gaagggtcctg tcctcctggg gacagtagtt acgggtggag aagtgaagaa gctgaagaga 180  
ctaacccttc agtttggtga tgcaagaaag gacagttctc tccacatcac tgcggcccag 240  
cctggtgata caggcctcta cctctgtgca ggagcgggaa gccaaaggaaa tctcatcttt 300  
ggaaaaggca cttaaactctc tgttaaacca aatatccaga accctgaccc tgccgtgtac 360  
cagctgagag actctaaatc cagtgaacag tctgtctgcc tattcaccga ttttgattct 420  
caaacaaatg tgtcacaag taaggattct gatgtgtata tcacagacaa aactgtgcta 480  
gacatgaggt ctatggactt caagagcaac agtgtgtgg cctggagcaa caaatctgac 540  
tttgcattgt caaacgcctt caacaacagc attattccag aagacacctt cttccccagc 600  
ccagaaagtt cccccggggg tagaatcgcc cggtggagg aaaaagtga aaccttgaaa 660  
gtcagaact cggagctggc gtccacggcc aacatgctca gggaacagggt ggcacagctt 720  
aaacagaaag tcatgaacta ctag 744

<210> 55

<211> 247

<212> PRT

<213> Homo sapiens

<220>

<223> Predicted amino acid sequence of soluble  
HLA-A2/flu matrix restricted TCR alpha chain from  
JM22, as fused to the leucine zipper domain of



human c-jun.

<400> 55

Met Gln Leu Leu Glu Gln Ser Pro Gln Phe Leu Ser Ile Gln Glu Gly  
1 5 10 15

Glu Asn Leu Thr Val Tyr Cys Asn Ser Ser Ser Val Phe Ser Ser Leu  
20 25 30

Gln Trp Tyr Arg Gln Glu Pro Gly Glu Gly Pro Val Leu Leu Val Thr  
35 40 45

Val Val Thr Gly Gly Glu Val Lys Lys Leu Lys Arg Leu Thr Phe Gln  
50 55 60

Phe Gly Asp Ala Arg Lys Asp Ser Ser Leu His Ile Thr Ala Ala Gln  
65 70 75 80

Pro Gly Asp Thr Gly Leu Tyr Leu Cys Ala Gly Ala Gly Ser Gln Gly  
85 90 95

Asn Leu Ile Phe Gly Lys Gly Thr Lys Leu Ser Val Lys Pro Asn Ile  
100 105 110

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser  
115 120 125

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val  
130 135 140

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu  
145 150 155 160

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser  
165 170 175

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile  
180 185 190

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Pro Gly Gly Arg  
195 200 205

Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser  
210 215 220

Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu  
225 230 235 240

Lys Gln Lys Val Met Asn Tyr  
245

<210> 56

<211> 864

<212> DNA  
<213> Homo sapiens

<220>

<223> DNA sequence of soluble soluble HLA-A2/flu matrix  
restricted TCR Beta chain from JM22, as fused to  
the leucine zipper domain of human c-fos.

<400> 56

```
atggtggatg gtggaatcac tcagtcccca aagtacctgt tcagaaagga aggacagaat 60
gtgaccctga gttgtgaaca gaatttgaac cacgatgcc a tgtactggta ccgacaggac 120
ccagggcaag ggctgagatt gatctactac tcacagatag taaatgactt tcagaaagga 180
gatatagctg aagggtacag cgtctctcgg gagaagaagg aatcctttcc tctcactgtg 240
acatcgcccc aaaagaaccc gacagctttc tatctctgtg ccagtagttc gaggagctcc 300
tacgagcagt acttcggggc gggcaccagg ctcacgggtc cagaggacct gaaaaacgtt 360
ttcccacccg aggtcgctgt gtttgaacca tcagaagcag agatctccca caccctaaag 420
gccacactgg tgtgcctggc cacaggcttc taccctgacc acgtggagct gagctgggtg 480
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagcccct caaggagcag 540
ccgcacctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc 600
tggcagaacc cccgcaacca ctcccgctgt caagtccagt tctacgggct ctcggagaat 660
gacgagtgga cccaggatag ggccaaacct gtcaccaga tctcagcgc cgaggcctgg 720
ggtagagcag accccggggg tctgactgat acactccaag cggagacaga tcaacttgaa 780
gacaagaagt ctgcgttgca gaccgagatt gccaatctac tgaaagagaa ggaaaaacta 840
gagttcatcc tggcagctta ctatg 864
```

<210> 57

<211> 287

<212> PRT

<213> Homo sapiens

<220>

<223> Predicted amino acid sequence of soluble  
HLA-A2/flu matrix restricted TCR Beta chain from  
JM22, as fused to the leucine zipper domain of  
human c-fos.

<400> 57

```
Met Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg Lys
 1             5             10             15

Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His Asp
      20             25             30

Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu Ile
      35             40             45

Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala Glu
      50             55             60

Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr Val
      65             70             75             80

Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser Ser
      85             90             95
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Ser | Ser | Tyr | Glu | Gln | Tyr | Phe | Gly | Pro | Gly | Thr | Arg | Leu | Thr | 100 | 105 | 110 |     |
| Val | Thr | Glu | Asp | Leu | Lys | Asn | Val | Phe | Pro | Pro | Glu | Val | Ala | Val | Phe | 115 | 120 | 125 |     |
| Glu | Pro | Ser | Glu | Ala | Glu | Ile | Ser | His | Thr | Gln | Lys | Ala | Thr | Leu | Val | 130 | 135 | 140 |     |
| Cys | Leu | Ala | Thr | Gly | Phe | Tyr | Pro | Asp | His | Val | Glu | Leu | Ser | Trp | Trp | 145 | 150 | 155 | 160 |
| Val | Asn | Gly | Lys | Glu | Val | His | Ser | Gly | Val | Ser | Thr | Asp | Pro | Gln | Pro | 165 | 170 | 175 |     |
| Leu | Lys | Glu | Gln | Pro | Ala | Leu | Asn | Asp | Ser | Arg | Tyr | Cys | Leu | Ser | Ser | 180 | 185 | 190 |     |
| Arg | Leu | Arg | Val | Ser | Ala | Thr | Phe | Trp | Gln | Asn | Pro | Arg | Asn | His | Phe | 195 | 200 | 205 |     |
| Arg | Cys | Gln | Val | Gln | Phe | Tyr | Gly | Leu | Ser | Glu | Asn | Asp | Glu | Trp | Thr | 210 | 215 | 220 |     |
| Gln | Asp | Arg | Ala | Lys | Pro | Val | Thr | Gln | Ile | Val | Ser | Ala | Glu | Ala | Trp | 225 | 230 | 235 | 240 |
| Gly | Arg | Ala | Asp | Pro | Gly | Gly | Leu | Thr | Asp | Thr | Leu | Gln | Ala | Glu | Thr | 245 | 250 | 255 |     |
| Asp | Gln | Leu | Glu | Asp | Lys | Lys | Ser | Ala | Leu | Gln | Thr | Glu | Ile | Ala | Asn | 260 | 265 | 270 |     |
| Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe | Ile | Leu | Ala | Ala | Tyr |     | 275 | 280 | 285 |     |

<210> 58

<211> 795

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence of soluble H2-Db/Influenza virus nucleoprotein restricted TCR beta chain from the murine F5 receptor, as fused to the leucine zipper domain of human c-fos.

<220>

<223> Description of Artificial Sequence: DNA sequence of soluble H2-Db/Influenza virus nucleoprotein restricted TCR beta chain from the murine F5 receptor, as fused to the leucine zipper domain of c-fos.

<400> 58

```
atgaactatt ctccagcttt agtgactgtg atgctgtttg tgtttgggag gacccatgga 60
gactcagtaa cccagatgca aggtcaagt accctctcag aagacgactt cctatttata 120
aactgtactt attcaaccac atggtacccg actcttttct ggtatgtcca atatcctgga 180
gaaggteccac agctcctttt gaaagtcaca acagccaaca acaagggaat cagcagaggt 240
tttgaagcta catatgataa aggaacaacg tccttccact tgcagaaagc ctcagtgcag 300
gagtcagact ctgctgtgta ctactgtgtg ctgggtgatc gacagggagg cagagctctg 360
atatttgga caggaaccac ggtatcagtc agccccaaca tccagaaccc agaacctgct 420
gtgtaccagt taaaagatcc tcggtctcag gacagcacc cctgcctgtt caccgacttt 480
gactcccaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcacac tgacaaaact 540
gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag 600
acaagcttca cctgccaaga tatctccaaa gagaccaacg ccacctacc cagttcagac 660
gttcccgagg gtagaatcgc ccggctggag gaaaaagtga aaaccttgaa agctcagaac 720
tcggagctgg cgtccacggc caacatgctc aggaacagg tggcacagct taaacagaaa 780
gtcatgaact actag 795
```

<210> 59

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted amino acid sequence of soluble  
H2-Db/Influenza virus nucleoprotein restricted TCR  
alpha chain from the murine F5 receptor, as fused  
to the leucine zipper domain of human c-jun.

<220>

<223> Description of Artificial Sequence: Predicted amino  
acid sequence of soluble H2-Db/Influenza virus  
nucleoprotein restricted TCR alpha chain from the  
murine F5 receptor, as fused to c-jun leucine  
zipper

<400> 59

```
Met Asn Tyr Ser Pro Ala Leu Val Thr Val Met Leu Phe Val Phe Gly
  1              5              10             15

Arg Thr His Gly Asp Ser Val Thr Gln Met Gln Gly Gln Val Thr Leu
      20              25             30

Ser Glu Asp Asp Phe Leu Phe Ile Asn Cys Thr Tyr Ser Thr Thr Trp
      35              40             45

Tyr Pro Thr Leu Phe Trp Tyr Val Gln Tyr Pro Gly Glu Gly Pro Gln
      50              55             60

Leu Leu Leu Lys Val Thr Thr Ala Asn Asn Lys Gly Ile Ser Arg Gly
      65              70             75             80

Phe Glu Ala Thr Tyr Asp Lys Gly Thr Thr Ser Phe His Leu Gln Lys
      85              90             95

Ala Ser Val Gln Glu Ser Asp Ser Ala Val Tyr Tyr Cys Val Leu Gly
```

|   |     |     |
|---|-----|-----|
| 100   | 105 | 110 |
| Asp Arg Gln Gly Gly Arg Ala Leu Ile Phe Gly Thr Gly Thr Thr Val |     |     |
| 115   | 120 | 125 |
| Ser Val Ser Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu |     |     |
| 130   | 135 | 140 |
| Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe |     |     |
| 145   | 150 | 155 |
| Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile |     |     |
| 165   | 170 | 175 |
| Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn |     |     |
| 180   | 185 | 190 |
| Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile |     |     |
| 195   | 200 | 205 |
| Ser Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Gly Gly |     |     |
| 210   | 215 | 220 |
| Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn |     |     |
| 225   | 230 | 235 |
| Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln |     |     |
| 245   | 250 | 255 |
| Leu Lys Gln Lys Val Met Asn Tyr                                 |     |     |
| 260   |     |     |

<210> 60  
 <211> 864  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DNA sequence  
 coding for soluble H2-Db/Influenza virus  
 nucleoprotein restricted TCR beta chain from the  
 murine F5 receptor, as fused to the c-fos leucine  
 zipper.

<400> 60  
 atgaaagctg gagttactca aactccaaga tatctgatca aaacgagagg acagcaagtg 60  
 acactgagct gctcccttat ctctgggcat aggagtgtat cctggtacca acagaccca 120  
 ggacagggcc ttcagttcct ctttgaatac ttcagtgaga cacagagaaa caaaggaaac 180  
 ttccctggtc gattctcagg gcgccagttc tctaactctc gctctgagat gaatgtgagc 240  
 accttgagc tgggggactc ggccctttat ctttgcgcca gcagcttcga cagcggaat 300  
 tcaccctcc actttgggaa cgggaccagg ctactgtga cagaggacct gaacaagggtg 360  
 ttcccaccg aggtcgctgt gtttgagcca tcagaagcag agatctcca caccaaaag 420  
 gccacactgg tgtgcctggc cacaggcttc ttccctgacc acgtggagct gagctggtgg 480

```

gtgaatggga aggaggtgca cagtgggggtc agccaggacc cgcagcccct caaggagcag 540
cccgccctca atgactccag atacagcctg agcagccgcc tgagggtctc ggccaccttc 600
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcgagagaat 660
gacgagtggg cccaggatag ggccaaacct gtcacccaga tcgtcagcgc cgaggcctgg 720
ggtagagcag accccggggg tctgactgat acaactccaag cggagacaga tcaacttgaa 780
gacaagaagt ctgcgttgca gaccgagatt gccaatctac tgaaagagaa ggaaaaacta 840
gagttcatcc tggcagctta ctac                                     864

```

<210> 61

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino acid  
sequence of soluble H2-Db/Influenza virus  
nucleoprotein restricted TCR beta chain from the  
murine F5 receptor, as fused to the c-fos leucine  
zipper.

<400> 61

```

Met Lys Ala Gly Val Thr Gln Thr Pro Arg Tyr Leu Ile Lys Thr Arg
 1             5             10             15

Gly Gln Gln Val Thr Leu Ser Cys Ser Pro Ile Ser Gly His Arg Ser
          20             25             30

Val Ser Trp Tyr Gln Gln Thr Pro Gly Gln Gly Leu Gln Phe Leu Phe
          35             40             45

Glu Tyr Phe Ser Glu Thr Gln Arg Asn Lys Gly Asn Phe Pro Gly Arg
          50             55             60

Phe Ser Gly Arg Gln Phe Ser Asn Ser Arg Ser Glu Met Asn Val Ser
          65             70             75             80

Thr Leu Glu Leu Gly Asp Ser Ala Leu Tyr Leu Cys Ala Ser Ser Phe
          85             90             95

Asp Ser Gly Asn Ser Pro Leu His Phe Gly Asn Gly Thr Arg Leu Thr
          100            105            110

Val Thr Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val Ala Val Phe
          115            120            125

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
          130            135            140

Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp
          145            150            155            160

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Gln Asp Pro Gln Pro
          165            170            175

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Lys | Glu | Gln | Pro | Ala | Leu | Asn | Asp | Ser | Arg | Tyr | Ser | Leu | Ser | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Leu | Arg | Val | Ser | Ala | Thr | Phe | Trp | Gln | Asn | Pro | Arg | Asn | His | Phe |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Cys | Gln | Val | Gln | Phe | Tyr | Gly | Leu | Ser | Glu | Asn | Asp | Glu | Trp | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Asp | Arg | Ala | Lys | Pro | Val | Thr | Gln | Ile | Val | Ser | Ala | Glu | Ala | Trp |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Arg | Ala | Asp | Pro | Gly | Gly | Leu | Thr | Asp | Thr | Leu | Gln | Ala | Glu | Thr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Gln | Leu | Glu | Asp | Lys | Lys | Ser | Ala | Leu | Gln | Thr | Glu | Ile | Ala | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe | Ile | Leu | Ala | Ala | Tyr |     |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

<210> 62

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence of soluble HLA-A2/HIV-1 Gag restricted TCR alpha chain from patient 003, as fused to the leucine zipper domain of human c-jun.

<400> 62

```

atgaaacaag aagttacaca gattcctgca gctctgagtg tcccagaagg agaaaacttg 60
gttctcaact gcagtttcac tgatagecgt atttacaacc tccagtgggt taggcaggac 120
cctgggaaag gtctcacatc tctgttgctt attcagtcaa gtcagagaga gcaaacaagt 180
ggaagactta atgcctcgct ggataaatca tcaggacgta gtactttata cattgcagct 240
tctcagcctg gtgactcagc cacctacctc tgtgctgtga ccaacttcaa caaattttac 300
tttggatctg ggaccaaact caatgtaaaa ccaaatatcc agaaccctga ccctgccgtg 360
taccagctga gagactctaa atccagtgc aagtctgtct gcctattcac cgattttgat 420
tctcaaacia atgtgtcaca aagtaaggat tctgatgtgt atatcacaga caaaactgtg 480
ctagacatga ggtctatgga cttcaagagc aacagtgtgt tggcctggag caacaaatct 540
gactttgcat gtgcaaacgc cttcaacaac agcattattc cagaagacac cttcttcccc 600
agcccagaaa gttcccccg gggtagaatc gcccggtg aggaaaaagt gaaaaccttg 660
aaagctcaga actcggagct ggcgtccacg gccaacatgc tcagggaaca ggtggcacag 720
cttaaacaga aagtcatgaa ctactag 747

```

<210> 63

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of soluble HLA-A2/HIV-1 Gag restricted  
TCR alpha chain from patient 003, as fused to the  
leucine zipper domain of human c-jun.

<400> 63

Met Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val Pro Glu  
1 5 10 15

Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala Ile Tyr  
20 25 30

Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr Ser Leu  
35 40 45

Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg Leu Asn  
50 55 60

Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile Ala Ala  
65 70 75 80

Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Thr Asn Phe  
85 90 95

Asn Lys Phe Tyr Phe Gly Ser Gly Thr Lys Leu Asn Val Lys Pro Asn  
100 105 110

Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser  
115 120 125

Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn  
130 135 140

Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val  
145 150 155 160

Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp  
165 170 175

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile  
180 185 190

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Pro Gly Gly  
195 200 205

Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn  
210 215 220

Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln  
225 230 235 240

Leu Lys Gln Lys Val Met Asn Tyr  
245



<210> 64  
 <211> 864  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
 of soluble HLA-A2/HIV-1 Gag restricted TCR beta  
 chain from patient 003, as fused to the leucine  
 zipper domain of human c-fos.

<400> 64

```

atgaaagctg gagttactca aactccaaga tatctgatca aaacgagagg acagcaagtg 60
acactgagct gctcccctat ctctgggcat aggagtgtat cctggtacca acagacccca 120
ggacagggcc ttcagtctct ctttgaatac ttcagtgaga cacagagaaa caaaggaaac 180
ttccctggtc gattctcagg gcgccagttc tctaactctc gctctgagat gaatgtgagc 240
accttggagc tgggggactc ggccctttat ctttgcgcca gcagcttcga cagcggggaat 300
tcacccctcc actttgggaa cgggaccagg ctcaactgtga cagaggacct gaacaagggtg 360
ttcccaccgc aggtcgctgt gtttgagcca tcagaagcag agatctccca caccaaaag 420
gccacactgg tgtgcctggc cacaggcttc ttccctgacc acgtggagct gagctggtgg 480
gtgaatggga aggaggtgca cagtggggtc agccaggacc cgcagcccct caaggagcag 540
cccgccctca atgactccag atacagcctg agcagccgcc tgagggtctc ggccaccttc 600
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat 660
gacgagtgga cccaggatag ggccaaacct gtcaccaga tcgtcagcgc cgaggcctgg 720
ggtagagcag accccggggg tctgactgat aactccaag cggagacaga tcaacttgaa 780
gacaagaagt ctgcgttgca gaccgagatt gccaatctac tgaaagagaa ggaaaaacta 840
gagttcatcc tggcagctta cttag                                     864
  
```

<210> 65  
 <211> 287  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
 sequence of soluble HLA-A2/HIV-1 Gag restricted  
 TCR beta chain from patient 003, as fused to the  
 leucine zipper domain of human c-fos.

<400> 65

```

Met Lys Ala Gly Val Thr Gln Thr Pro Arg Tyr Leu Ile Lys Thr Arg
  1             5             10             15

Gly Gln Gln Val Thr Leu Ser Cys Ser Pro Ile Ser Gly His Arg Ser
          20             25             30

Val Ser Trp Tyr Gln Gln Thr Pro Gly Gln Gly Leu Gln Phe Leu Phe
      35             40             45

Glu Tyr Phe Ser Glu Thr Gln Arg Asn Lys Gly Asn Phe Pro Gly Arg
      50             55             60

Phe Ser Gly Arg Gln Phe Ser Asn Ser Arg Ser Glu Met Asn Val Ser
  
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Thr | Leu | Glu | Leu | Gly | Asp | Ser | Ala | Leu | Tyr | Leu | Cys | Ala | Ser | Ser | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ser | Gly | Asn | Ser | Pro | Leu | His | Phe | Gly | Asn | Gly | Thr | Arg | Leu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Thr | Glu | Asp | Leu | Asn | Lys | Val | Phe | Pro | Pro | Glu | Val | Ala | Val | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Pro | Ser | Glu | Ala | Glu | Ile | Ser | His | Thr | Gln | Lys | Ala | Thr | Leu | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Leu | Ala | Thr | Gly | Phe | Phe | Pro | Asp | His | Val | Glu | Leu | Ser | Trp | Trp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Val | Asn | Gly | Lys | Glu | Val | His | Ser | Gly | Val | Ser | Gln | Asp | Pro | Gln | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Lys | Glu | Gln | Pro | Ala | Leu | Asn | Asp | Ser | Arg | Tyr | Ser | Leu | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Leu | Arg | Val | Ser | Ala | Thr | Phe | Trp | Gln | Asn | Pro | Arg | Asn | His | Phe |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Cys | Gln | Val | Gln | Phe | Tyr | Gly | Leu | Ser | Glu | Asn | Asp | Glu | Trp | Thr |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Gln | Asp | Arg | Ala | Lys | Pro | Val | Thr | Gln | Ile | Val | Ser | Ala | Glu | Ala | Trp |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Gly | Arg | Ala | Asp | Pro | Gly | Gly | Leu | Thr | Asp | Thr | Leu | Gln | Ala | Glu | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Gln | Leu | Glu | Asp | Lys | Lys | Ser | Ala | Leu | Gln | Thr | Glu | Ile | Ala | Asn |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Leu | Lys | Glu | Lys | Glu | Lys | Leu | Glu | Phe | Ile | Leu | Ala | Ala | Tyr |     |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

<210> 66

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence of soluble HLA-A2/HTLV-1 Tax restricted TCR alpha chain from clone A6, as fused to the leucine zipper domain of c-jun.

<400> 66

```

atgcagaagg aagtggagca gaactctgga cccctcagtg ttccagaggg agccattgcc 60
tctctcaact gcacttacag tgaccgaggt tcccagtcct tcttctggta cagacaatat 120
tctgggaaaa gccctgagtt gataatgtcc atatactcca atggtgacaa agaagatgga 180
aggtttacag cacagctcaa taaagccagc cagtatgttt ctctgctcat cagagactcc 240
cagcccagtg attcagccac ctacctctgt gccgttacaa ctgacagctg ggggaaattg 300
cagtttgtag cagggacca ggttggtggtc accccagata tccagaacct tgacctgcc 360
gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt 420
gattctcaaa caaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact 480
gtgctagaca tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa 540
tctgactttg catgtgcaaa cgcttcaac aacagcatta ttccagaaga caccttcttc 600
cccagcccag aaagttcccc cgggggtaga atcgcccggc tggaggaaaa agtgaacc 660
ttgaaagctc agaactcgga gctggcgtcc acggccaaca tgctcaggga acaggtggca 720
cagcttaaac agaaagtcac gaactactag 750

```

<210> 67

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of soluble HLA-A2/HTLV-1 Tax restricted TCR alpha chain from clone A6, as fused to the leucine zipper domain of c-jun.

<400> 67

```

Met Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu
  1             5             10            15

Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln
          20             25            30

Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile
      35             40            45

Met Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala
      50             55            60

Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser
      65             70            75            80

Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Thr Thr Asp Ser
          85             90            95

Trp Gly Lys Leu Gln Phe Gly Ala Gly Thr Gln Val Val Val Thr Pro
      100            105            110

Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys
      115            120            125

Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr
      130            135            140

Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr

```

|   |     |     |     |
|---|-----|-----|-----|
| 145   | 150 | 155 | 160 |
| Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala |     |     |     |
|   | 165 | 170 | 175 |
| Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser |     |     |     |
|   | 180 | 185 | 190 |
| Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Pro Gly |     |     |     |
|   | 195 | 200 | 205 |
| Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln |     |     |     |
|   | 210 | 215 | 220 |
| Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala |     |     |     |
|   | 225 | 230 | 235 |
| Gln Leu Lys Gln Lys Val Met Asn Tyr                             |     |     |     |
|   | 245 |     |     |

<210> 68

<211> 928

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence of soluble HLA-A2/HTLV-1 Tax restricted TCR beta chain from clone A6, as fused to the leucine zipper domain of c-fos and a BirA biotinylation tag.

<400> 68

```

atgaacgctg gtgtcactca gacccccaaaa ttccaggtcc tgaagacagg acagagcatg 60
aactgacagt gtgcccagga tatgaaccat gaatacatgt cctgggtatcg acaagaccca 120
ggcatggggc tgaggctgat tcattactca gttgggtgctg gtatcactga ccaaggagaa 180
gtccccaatg gctacaatgt ctccagatca accacagagg atttcccgtc caggctgctg 240
tcggctgctc cctcccagac atctgtgtac ttctgtgcca gcaggccggg actagcggga 300
gggcgaccag agcagtactt cgggccgggc accaggctca cggtcacaga ggacctgaaa 360
aacgtgttcc caccagaggt cgtgtgtgtt gagccatcag aagcagagat ctcccacacc 420
caaaaggcca cactggtgtg cctggccaca ggcttctacc ccgaccacgt ggagctgagc 480
tggtgggtga atgggaagga ggtgcacagt ggggtcagca cagacccgca gcccctcaag 540
gagcagcccg ccctcaatga ctccagatac gctctgagca gccgcctgag ggtctcggcc 600
accttctggc agaacccccg caaccacttc cgctgtcaag tccagttcta cgggctctcg 660
gagaatgacg agtggacca ggatagggcc aaacctgtca ccagatcgt cagcgccgag 720
gcctggggta gagcagaccc cgggggtctg actgatacac tccaagcgga gacagatcaa 780
cttgaagaca agaagtctgc gttgcagacc gagattgcca atctactgaa agagaaggaa 840
aaactagagt tcatcctggc agcttaacga tccgggtggtg gtctgaacga tatttttgaa 900
gctcagaaaa tcgaatggca ttaagctt                                     928

```

<210> 69

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of soluble HLA-A2/HTLV-1 Tax restricted  
TCR beta chain from clone A6, as fused to the  
leucine zipper domain of c-fos and a BirA  
biotinylation ta

<400> 69

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ala | Gly | Val | Thr | Gln | Thr | Pro | Lys | Phe | Gln | Val | Leu | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gln | Ser | Met | Thr | Leu | Gln | Cys | Ala | Gln | Asp | Met | Asn | His | Glu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ser | Trp | Tyr | Arg | Gln | Asp | Pro | Gly | Met | Gly | Leu | Arg | Leu | Ile | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ser | Val | Gly | Ala | Gly | Ile | Thr | Asp | Gln | Gly | Glu | Val | Pro | Asn | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Asn | Val | Ser | Arg | Ser | Thr | Thr | Glu | Asp | Phe | Pro | Leu | Arg | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ala | Ala | Pro | Ser | Gln | Thr | Ser | Val | Tyr | Phe | Cys | Ala | Ser | Arg | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Leu | Ala | Gly | Gly | Arg | Pro | Glu | Gln | Tyr | Phe | Gly | Pro | Gly | Thr | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Val | Thr | Glu | Asp | Leu | Lys | Asn | Val | Phe | Pro | Pro | Glu | Val | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Phe | Glu | Pro | Ser | Glu | Ala | Glu | Ile | Ser | His | Thr | Gln | Lys | Ala | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Cys | Leu | Ala | Thr | Gly | Phe | Tyr | Pro | Asp | His | Val | Glu | Leu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Trp | Trp | Val | Asn | Gly | Lys | Glu | Val | His | Ser | Gly | Val | Ser | Thr | Asp | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Pro | Leu | Lys | Glu | Gln | Pro | Ala | Leu | Asn | Asp | Ser | Arg | Tyr | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Arg | Leu | Arg | Val | Ser | Ala | Thr | Phe | Trp | Gln | Asn | Pro | Arg | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Phe | Arg | Cys | Gln | Val | Gln | Phe | Tyr | Gly | Leu | Ser | Glu | Asn | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Trp | Thr | Gln | Asp | Arg | Ala | Lys | Pro | Val | Thr | Gln | Ile | Val | Ser | Ala | Glu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Ala Trp Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala  
245 250 255

Glu Thr Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile  
260 265 270

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
275 280 285

Tyr Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile  
290 295 300

Glu Trp His  
305

<210> 70  
<211> 765  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequence of  
soluble HLA-A2/HTLV-1 Tax restricted TCR alpha  
chain from clone M10B7/D3, as fused to the leucine  
zipper domain of c-jun.

<400> 70  
atgcaacaga agaatgatga ccagcaagtt aagcaaaatt caccatccct gagcggtccag 60  
gaaggaagaa tttctattct gaactgtgac tatactaaca gcatgtttga ttatttccta 120  
tggtacaaaa aataccctgc tgaaggtect acattcctga tatctataag ttccattaag 180  
gataaaaatg aagatggaag attcactgtc ttcttaaaca aaagtgccaa gcacctctct 240  
ctgcacattg tgccctccca gcctggagac tctgcagtgt acttctgtgc agcaatggag 300  
ggagcccaga agctggtatt tggccaagga accaggctga ctatcaaccc aaatatccag 360  
aaccctgacc ctgccgtgta ccagctgaga gactctaaat ccagtgacaa gtctgtctgc 420  
ctattcaccg attttgattc tcaaacaaat gtgtcacaaa gtaaggattc tgatgtgtat 480  
atcacagaca aaactgtgct agacatgagg tctatggact tcaagagcaa cagtgtctgtg 540  
gcctggagca acaaactctga ctttgcatgt gcaaacgcct tcaacaacag cattattcca 600  
gaagacacct tcttccccag ccagaaaagt tccccgggg gtagaatcgc ccggctggag 660  
gaaaaagtga aaaccttgaa agctcagaac tcggagctgg cgtccacggc caacatgctc 720  
agggaaacag tggcacagct taaacagaaa gtcatgaact actag 765

<210> 71  
<211> 254  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequence of  
soluble HLA-A2/HTLV-1 Tax restricted TCR alpha  
chain from clone M10B7/D3, as fused to the leucine  
zipper domain of c-jun.

<400> 71

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Gln | Lys | Asn | Asp | Asp | Gln | Gln | Val | Lys | Gln | Asn | Ser | Pro | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Ser | Val | Gln | Glu | Gly | Arg | Ile | Ser | Ile | Leu | Asn | Cys | Asp | Tyr | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Ser | Met | Phe | Asp | Tyr | Phe | Leu | Trp | Tyr | Lys | Lys | Tyr | Pro | Ala | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Pro | Thr | Phe | Leu | Ile | Ser | Ile | Ser | Ser | Ile | Lys | Asp | Lys | Asn | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Gly | Arg | Phe | Thr | Val | Phe | Leu | Asn | Lys | Ser | Ala | Lys | His | Leu | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | His | Ile | Val | Pro | Ser | Gln | Pro | Gly | Asp | Ser | Ala | Val | Tyr | Phe | Cys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |
| Ala | Ala | Met | Glu | Gly | Ala | Gln | Lys | Leu | Val | Phe | Gly | Gln | Gly | Thr | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Thr | Ile | Asn | Pro | Asn | Ile | Gln | Asn | Pro | Asp | Pro | Ala | Val | Tyr | Gln |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Arg | Asp | Ser | Lys | Ser | Ser | Asp | Lys | Ser | Val | Cys | Leu | Phe | Thr | Asp |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Phe | Asp | Ser | Gln | Thr | Asn | Val | Ser | Gln | Ser | Lys | Asp | Ser | Asp | Val | Tyr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ile | Thr | Asp | Lys | Thr | Val | Leu | Asp | Met | Arg | Ser | Met | Asp | Phe | Lys | Ser |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asn | Ser | Ala | Val | Ala | Trp | Ser | Asn | Lys | Ser | Asp | Phe | Ala | Cys | Ala | Asn |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ala | Phe | Asn | Asn | Ser | Ile | Ile | Pro | Glu | Asp | Thr | Phe | Phe | Pro | Ser | Pro |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Ser | Ser | Pro | Gly | Gly | Arg | Ile | Ala | Arg | Leu | Glu | Glu | Lys | Val | Lys |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Thr | Leu | Lys | Ala | Gln | Asn | Ser | Glu | Leu | Ala | Ser | Thr | Ala | Asn | Met | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Arg | Glu | Gln | Val | Ala | Gln | Leu | Lys | Gln | Lys | Val | Met | Asn | Tyr |     |     |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |  |

<210> 72

<211> 925

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence of soluble HLA-A2/HTLV-1 Tax restricted TCR beta chain from clone M10B7/D3, as fused to the leucine zipper domain of c-fos and a BirA biotinylation tag

<400> 72

```
atgaacgctg gtgtcactca gacccccaaa ttccaggtcc tgaagacagg acagagcatg 60
acactgcagt gtgccagga tatgaaccat gaatacatgt cctggatatcg acaagaccca 120
ggcatggggc tgaggctgat tcattactca gttgggtgctg gtatcactga ccaaggagaa 180
gtccccaatg gctacaatgt ctccagatca accacagagg atttcccgtc caggctgctg 240
tcggctgctc cctcccagac atctgtgtac ttctgtgcca gcagttacca ggaggggggg 300
ttttacgagc agtacttcgg gccgggcacc aggctcacgg tcacagagga cctgaaaaac 360
gtgttccac ccgaggtcgc tgtgtttgag ccatacagaag cagagatctc ccacacccaa 420
aaggccacac tgggtgtgct ggccacaggg ttctaccccg accacgtgga gctgagctgg 480
tggtgtaatg ggaaggaggt gcacagtggg gtcagcacag acccgagcc cctcaaggag 540
cagcccgccc tcaatgactc cagatacgtc ctgagcagcc gcctgagggt ctcgccacc 600
ttctggcagg acccccgcaa ccacttcgc tgtcaagtcc agttctacgg gctctcggag 660
aatgacgagt ggaccagga tagggccaaa cccgtcacc agatcgtcag cgccgaggcc 720
tggtgtagag cagaccccg ggtctgact gatacactcc aagcgagac agatcaactt 780
gaagacaaga agtctgcgtt gcagaccgag attgccaatc tactgaaaga gaaggaaaaa 840
ctagagttca tctggcagc ttacggatcc ggtggtggtc tgaacgatat ttttgaagct 900
cagaaaatcg aatggcatta agctt 925
```

<210> 73

<211> 306

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of soluble HLA-A2/HTLV-1 Tax restricted TCR beta chain from clone M10B7/D3, as fused to the c-fos leucine zipper domain and a BirA biotinylation tag.

<400> 73

```
Met Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr
 1             5             10            15

Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr
      20             25             30

Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His
      35             40             45

Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn Gly
      50             55             60

Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu
      65             70             75             80

Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr
```





c-fos leucine zipper domain and a BirA  
biotinylation tag.

<400> 74

```

atgaacgctg gtgtcactca gacccccaaaa ttccagggtcc tgaagacagg acagagcatg 60
aactgcagt gtgcccagga tatgaacccat gaatacatgt cctgggtatcg acaagaccca 120
ggcatggggc tgaggctgat tcattactca gttgggtgctg gtatcactga ccaaggagaa 180
gtccccaatg gctacaatgt ctccagatca accacagagg atttcccgt caggctgctg 240
tcggctgctc cctcccagac atctgtgtac ttctgtgcca gcaggccggg actagcggga 300
gggcgaccag agcagtactt cgggcccgggc accagggtca cggtcacaga ggacctgaaa 360
aacgtgttcc caccgaggt cgctgtgttt gagccatcag aagcagagat ctcccacacc 420
caaaaggcca cactggtgtg cctggccaca ggcttctacc ccgaccacgt ggagctgagc 480
tggtgggtga atgggaagga ggtgcacagt ggggtcagca cagaccgcga gccctcaag 540
gagcagcccg cctcaatga ctccagatac gctctgagca gccgcctgag ggtctcggcc 600
accttctggc aggacccccg caaccacttc cgctgtcaag tccagttcta cgggctctcg 660
gagaatgacg agtggaccca ggatagggcc aaacctgtca cccagatcgt cagcgccgag 720
gcctggggta gagcagaccc cgggggtctg actgatacac tccaagcgga gacagatcaa 780
cttgaagaca agaagtctgc gttgcagacc gagattgcca atctactgaa agagaaggaa 840
aaactagagt tcatcctggc agcttacgga tccgggtggtg gtctgaacga tatttttgaa 900
gctcagaaaa tcgaatggca ttaagctt 928

```

<210> 75

<211> 307

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of  
mutated soluble HLA-A2/HTLV-1 Tax restricted TCR  
beta chain from clone A6, as fused to the c-fos  
leucine zipper domain and a BirA biotinylation  
tag.

<400> 75

```

Met Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys Thr
  1              5              10              15

Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu Tyr
      20              25              30

Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile His
      35              40              45

Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn Gly
      50              55              60

Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu
      65              70              75              80

Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser Arg Pro
      85              90              95

Gly Leu Ala Gly Gly Arg Pro Glu Gln Tyr Phe Gly Pro Gly Thr Arg
      100              105              110

```

Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala  
 115 120 125  
 Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr  
 130 135 140  
 Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser  
 145 150 155 160  
 Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro  
 165 170 175  
 Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Ala Leu  
 180 185 190  
 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asp Pro Arg Asn  
 195 200 205  
 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu  
 210 215 220  
 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu  
 225 230 235 240  
 Ala Trp Gly Arg Ala Asp Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala  
 245 250 255  
 Glu Thr Asp Gln Leu Glu Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile  
 260 265 270  
 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala  
 275 280 285  
 Tyr Gly Ser Gly Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile  
 290 295 300  
 Glu Trp His  
 305

<210> 76

<211> 190

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence  
 of the c-fos/BirA biotinylation tag fusion partner  
 used for TCR beta chains.

<400> 76

cccggggggtc tgactgatac actccaagcg gagacagatc aacttgaaga caagaagtct 60  
 gcgttgacaga ccgagattgc caatctactg aaagagaagg aaaaactaga gttcatcctg 120  
 gcagcttacg gatccggtgg tggctctgaac gatatttttg aagctcagaa aatcgaatgg 180

<210> 77  
<211> 61  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequence of  
the c-fos/BirA biotinylation tag fusion partner  
used for TCR beta chains.

<400> 77  
Pro Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu  
1 5 10 15  
Asp Lys Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu  
20 25 30  
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala Tyr Gly Ser Gly Gly Gly  
35 40 45  
Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His  
50 55 60

<210> 78  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Reverse primer  
used for PCR amplification of the Vbeta-c-fos  
leucine zipper fragment of the Influenza matrix  
peptide/HLA-A0201 restricted human JM22 TCR fusion  
gene

<400> 78  
acaacacggat ccgtaagctg cgacgatgaa ctcgatcttc tt

42

<210> 79  
<211> 90  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer for PCR  
amplification of the human Vbeta17 chain of the  
JM22 TCR fused to the Bir biotinylation tag.

<400> 79

gggggaagct taatgccatt cgattttctg agcttcaaaa atatcggttca gaccaccacc 60  
ggatccgtaa gctgccagga tgaactctag 90

<210> 80  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer for PCR  
amplification of the human Vbeta17 chain of the  
JM22 TCR fused to the Bir biotinylation tag.

<400> 80  
gctctagaca tatgggccca gtggattctg gagtcac 37

<210> 81  
<211> 9  
<212> PRT  
<213> Human immunodeficiency virus

<220>  
<223> Peptide derived from the HIV-1 Reverse  
Transcriptase protein and presented as peptide  
antigen by HLA-A0201.

<400> 81  
Ile Leu Lys Glu Pro Val His Gly Val  
1 5

<210> 82  
<211> 9  
<212> PRT  
<213> Human T-cell lymphotropic virus type 1

<220>  
<223> Peptide derived from the HTLV-1 Tax protein and  
presented as peptide antigen by HLA-A0201. This  
HLA/peptide combination restricts the A6 and B7  
TCRs.

<400> 82  
Leu Leu Phe Gly Tyr Pro Val Tyr Val  
1 5

<210> 83  
<211> 9  
<212> PRT  
<213> Influenza virus

<220>

<223> Peptide derived from Influenza virus nucleoprotein and presented as peptide antigen by the murine H2-Db. This MHC/peptide combination restricted the murine F5 TCR.

<400> 83

Ala Ser Asn Glu Asn Met Asp Ala Met  
1 5

<210> 84

<211> 9

<212> PRT

<213> Influenza virus

<220>

<223> Peptide derived from Influenza virus Matrix protein and presented as peptide antigen by HLA-A0201. This HLA/peptide combination restricted the JM22TCR.

<400> 84

Gly Ile Leu Gly Phe Val Phe Thr Leu  
1 5

<210> 85

<211> 9

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> Peptide derived from HIV-1 Gag protein and presented as peptide antigen by HLA-A0201. This HLA/peptide combination restrictes the TCR cloned from patient 003.

<400> 85

Ser Leu Tyr Asn Thr Val Ala Thr Leu  
1 5